

Amendments to the Claims:

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims

Claim 1. (currently amended) A system for high throughput detection of genotypes comprising

a sample preparation method;

a sample preparation automation system;

a sample tracking system;

an automated high density probe array loader;

a computer system for managing hybridization data and for analyzing hybridization data to make genotype calls.

Claim 2. (currently amended) The system of Claim 1 wherein the sample preparation automation system is a robotic device for handling ~~multwell~~ multiwell plates.

Claim 3. (original) The system of Claim 1 wherein the sample tracking system is a bar code system.

Claim 4. (currently amended) The system of Claim 1 wherein computer system comprises a processor; and a memory being coupled with the processor, the memory storing a plurality of machine instructions that cause the processor to perform the method step of analyzing the hybridization to determine the genotype; ~~wherein the analyzing comprises calling a genotype by calculating the likelihood of a set of models for the hybridization and the base is called based upon the likelihood of the models; wherein the distribution of hybridization intensities are assumed to be Gaussein and forward and reverse strand are treated as independent replicates.~~

Claims 5-14. (canceled)

Claim 15 (new) The system of claim 1 wherein two laboratory personnel working for one day can obtain genotype calls for at least 1.4 megabases of sequence.

Claim 16 (new) The system of claim 1 wherein two laboratory personnel genotype at least 35 kilobases of sequence from each of at least 40 samples in one day.

Claim 17 (new) The system of claim 1 wherein the sample tracking system and the computer system are linked.

Claim 18 (new) The system of claim 1 wherein the sample preparation method comprises long range PCR amplification of a plurality of nucleic acid samples.

Claim 19 (new) The system of claim 18 wherein the amplicons obtained after long range PCR amplification are from 3 to 15 kilobases.

Claim 20 (new) The system of claim 18 wherein prior to PCR amplification each nucleic acid sample is reverse transcribed to obtain cDNA.

Claim 21 (new) The system of claim 1 wherein hybridization data is obtained by hybridizing nucleic acid samples to high density nucleic acid probe arrays wherein said probe arrays have feature sizes of about 20 x 24 microns or smaller.

Claim 22 (new) The system of claim 21 wherein each high density nucleic acid probe array is capable of simultaneous screening of at least 30 kilobases of sense nucleic acid sequence and at least 30 kb of antisense nucleic acid sequence.

Claim 23 (new) The system of claim 21 wherein the high density nucleic acid probe arrays are resequencing or variation detection arrays.

Claim 24 (new) The system of claim 21 wherein the high density nucleic acid probe arrays genotype a plurality of single nucleotide polymorphisms.

Claim 25 (new) The system of claim 21 wherein a contiguous sequence is tiled on the high density nucleic acid probe arrays.

Claim 26 (new) The system of claim 1 wherein the sample tracking system comprises a single or multiple dimensional barcode system.

Claim 27 (new) The system of claim 1 wherein the sample tracking system comprises an electromagnetic encoding system.